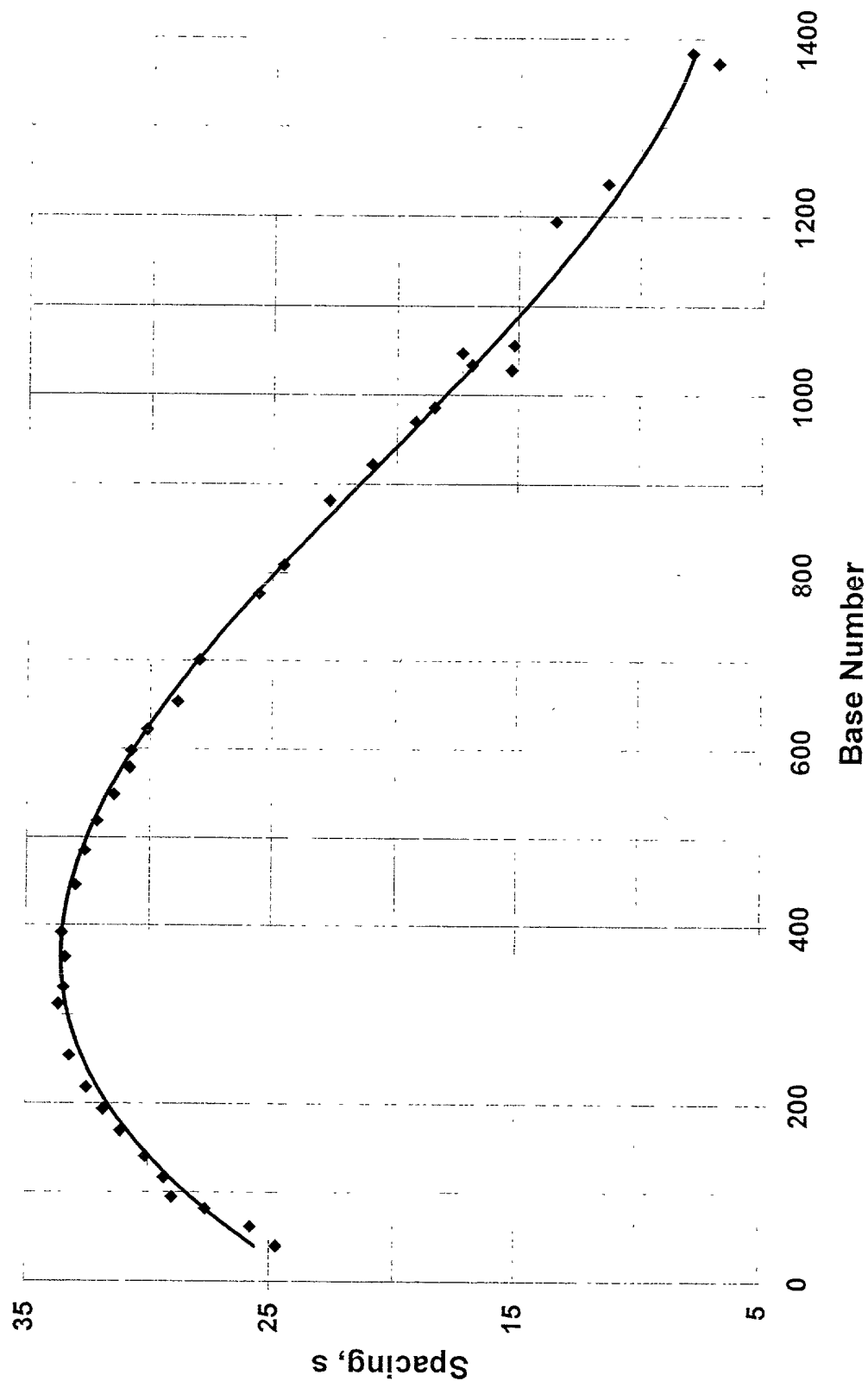
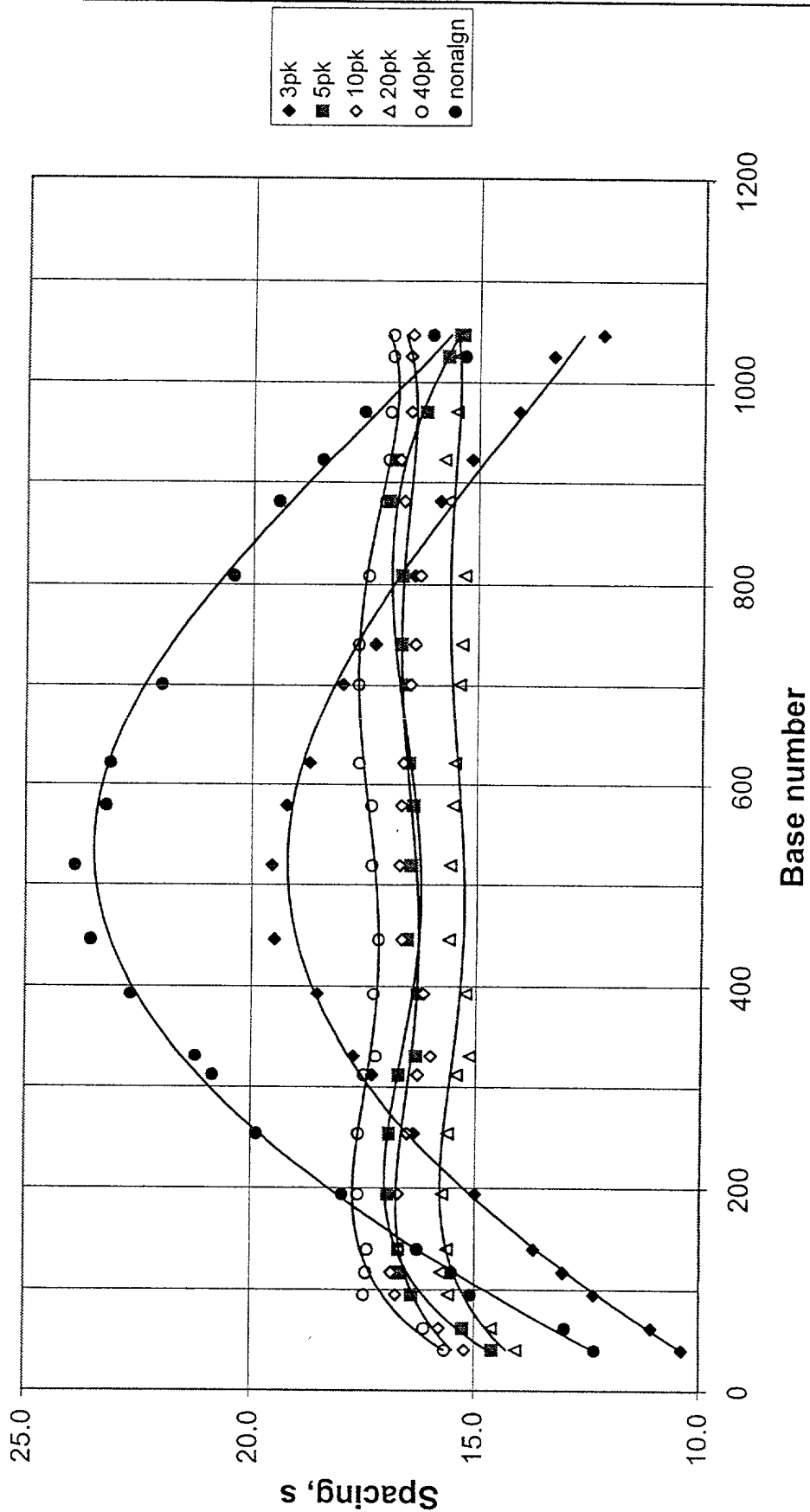


Spacing Between Adjacent Peaks in the Raw Data
(M13, T's T=6%, 60C, Long Gel)



Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data)
(M13, Long Gel, 55C, T=6%)



Standard Deviation (%) of the Spacing Between Adjacent Bases from
Average as a Function of Number of Peaks Used as a Reference for
Alignment of Raw Data

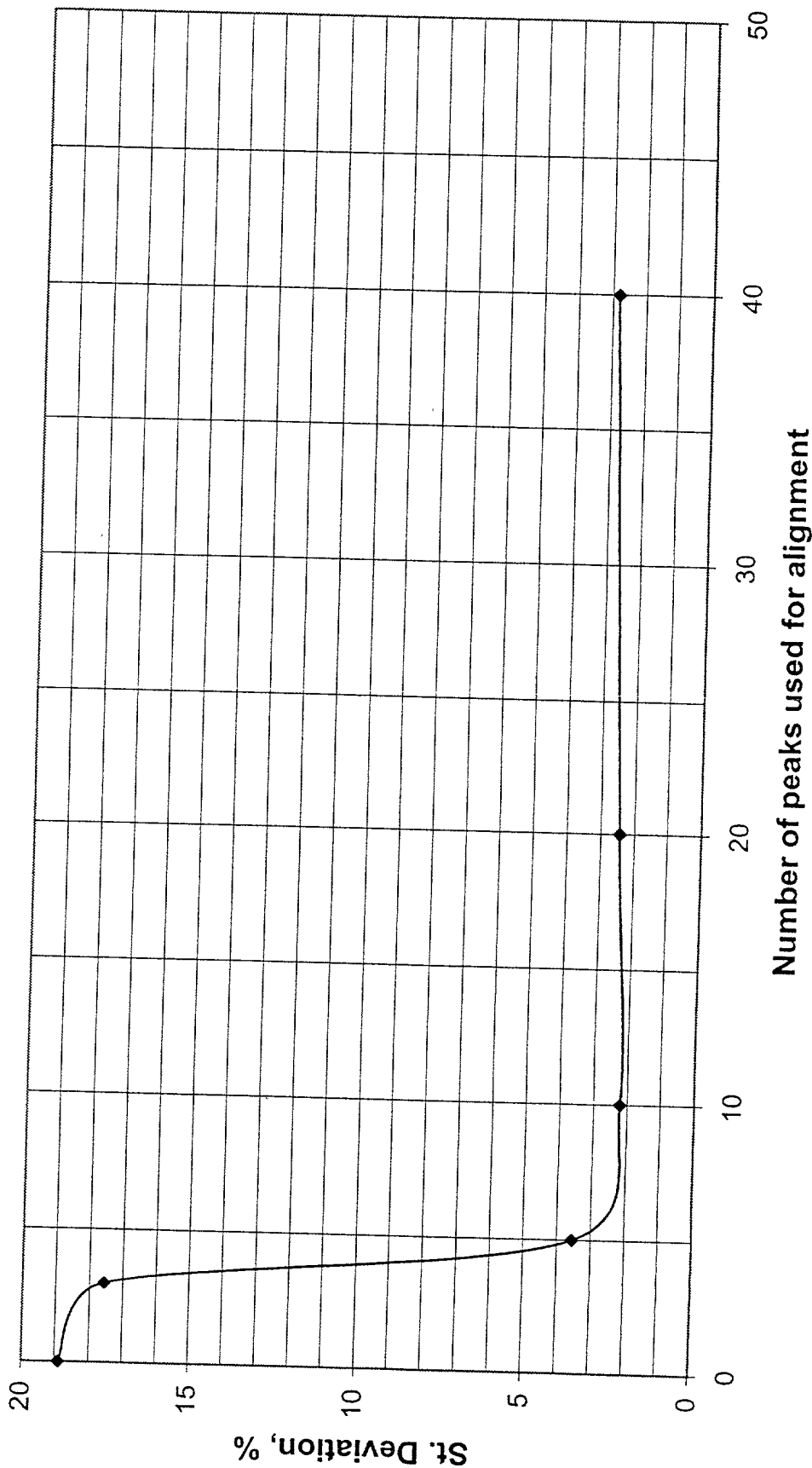
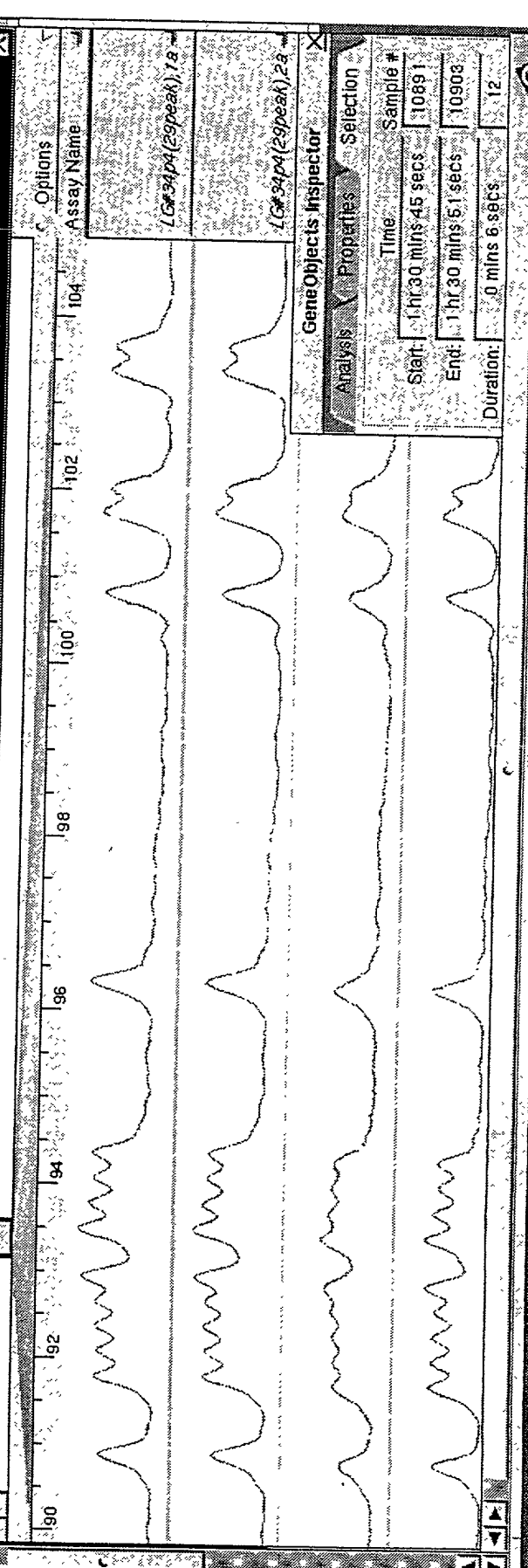


Fig. 4

TOC 2000
peak312raw.tiff -- /Data/LongGal/LG#34/Seq1



peak312alignment.tiff -- /Data/LongGal/LG#34/Seq1

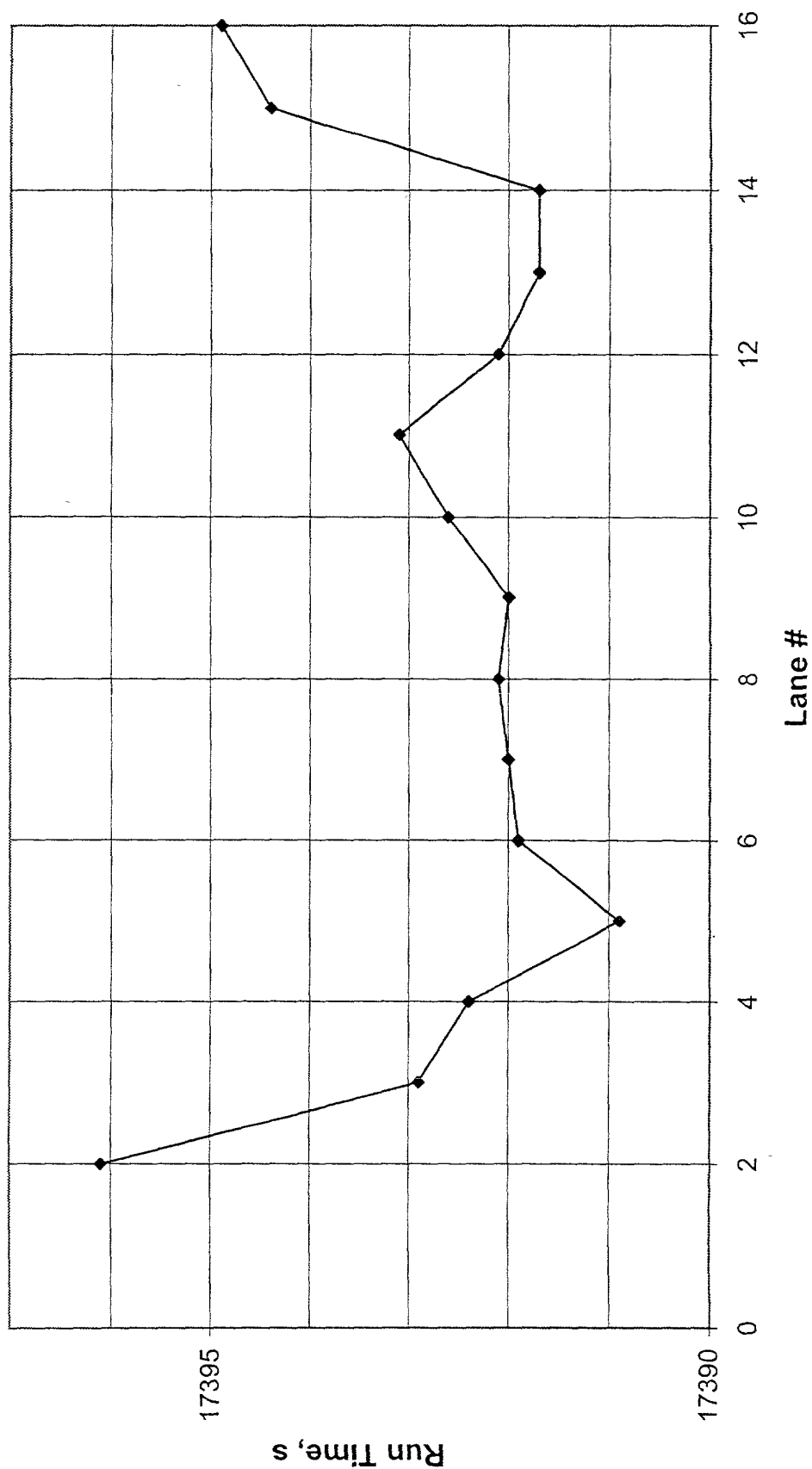


Buttons: Preview, Stop, Run, and a small icon.

FS 4

103070 2242300

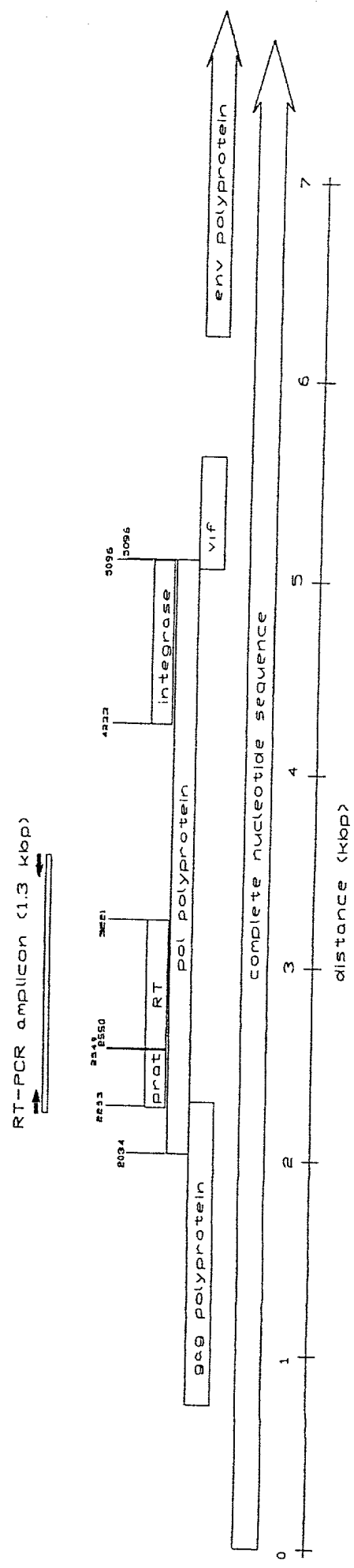
Run Time of the BP#1056 in Different Lanes
(after alignment based on 10 peaks)



175

175

Figure 6

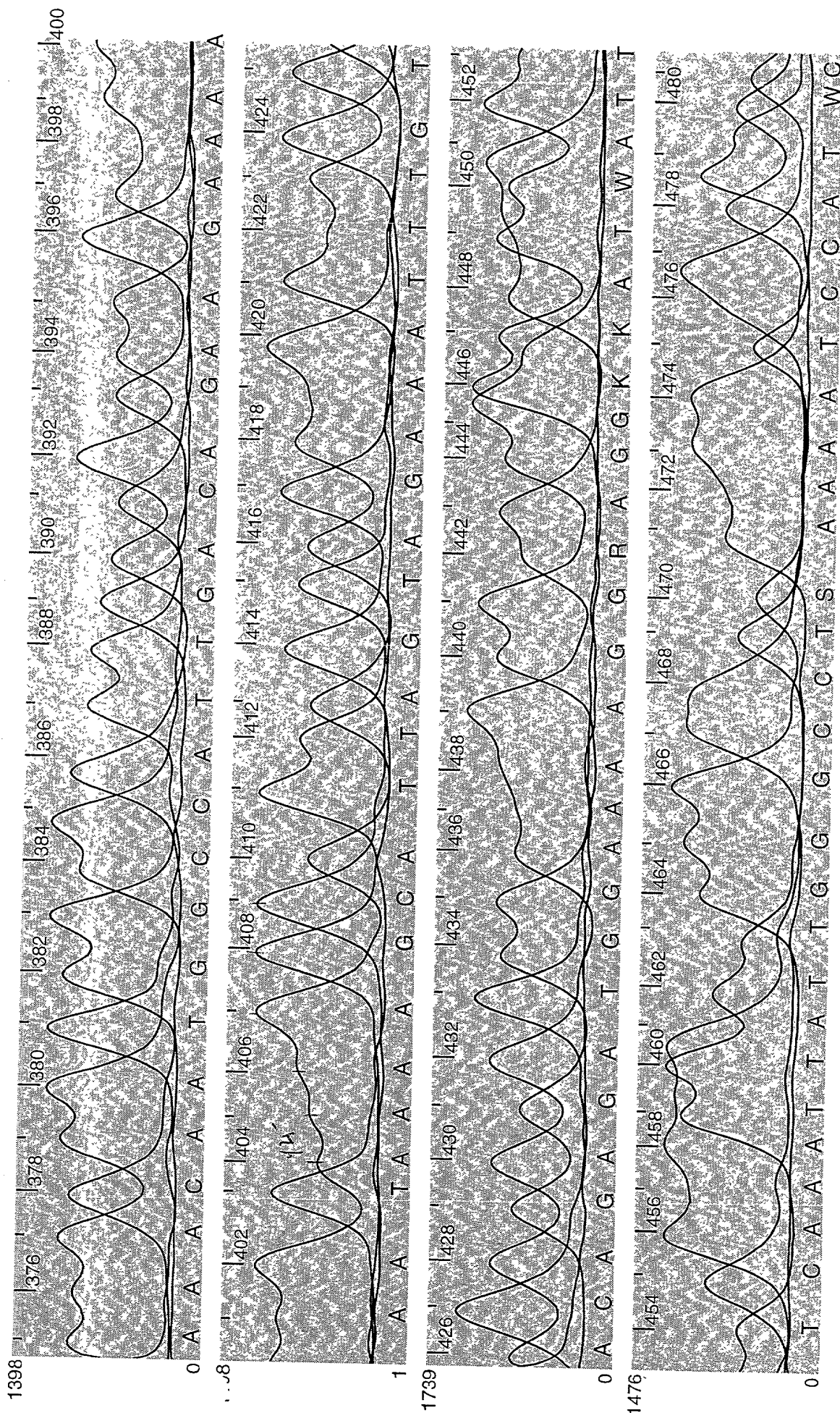


157



TOSONO" 2242360

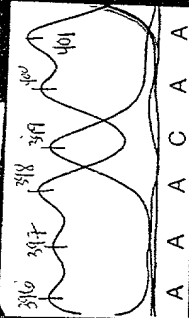
Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc



Assay Notes: Long CLIP with RT-PCR of RNA tyophilized with Glycine+ NaAc

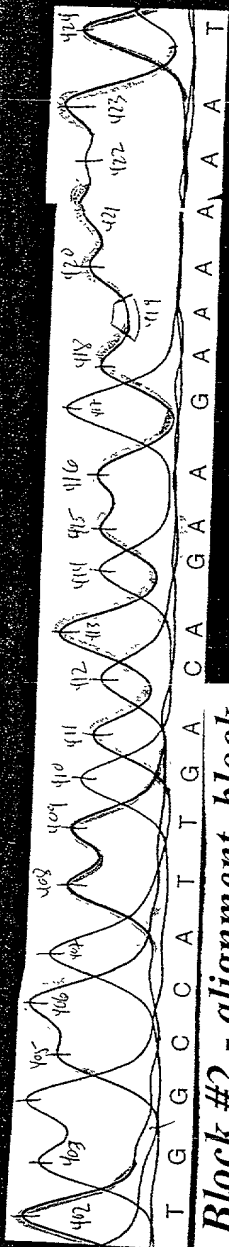
Reference Bands

Block #1 -

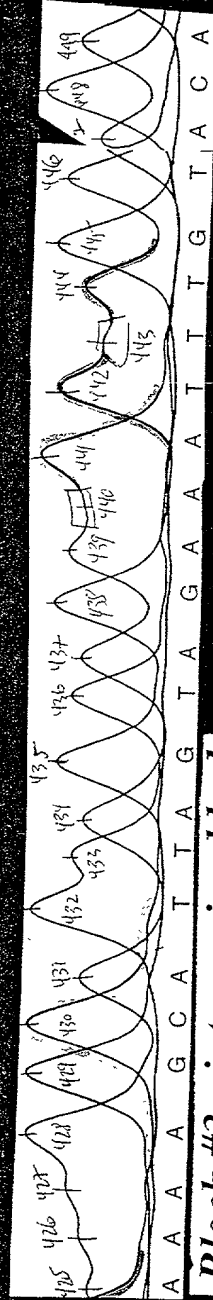


intervening block

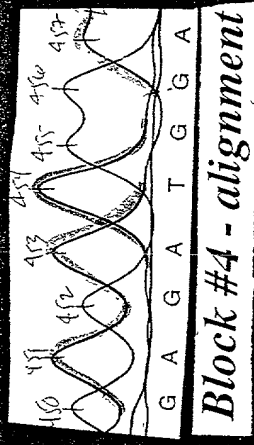
Block #2 - alignment block



Block #3 - intervening block



Block #4 - alignment block





Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

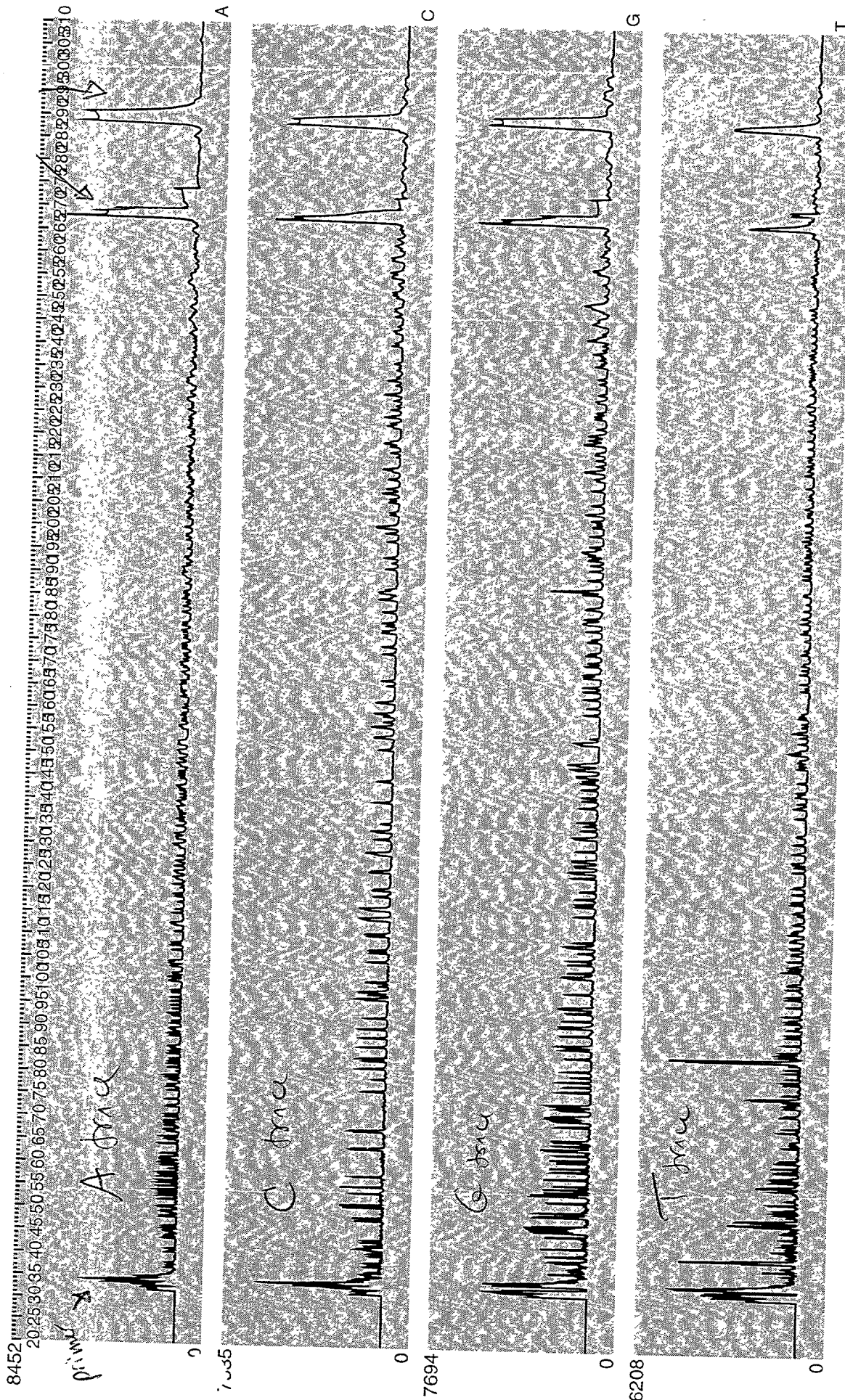


Figure 9A



UCRL-2000-2000

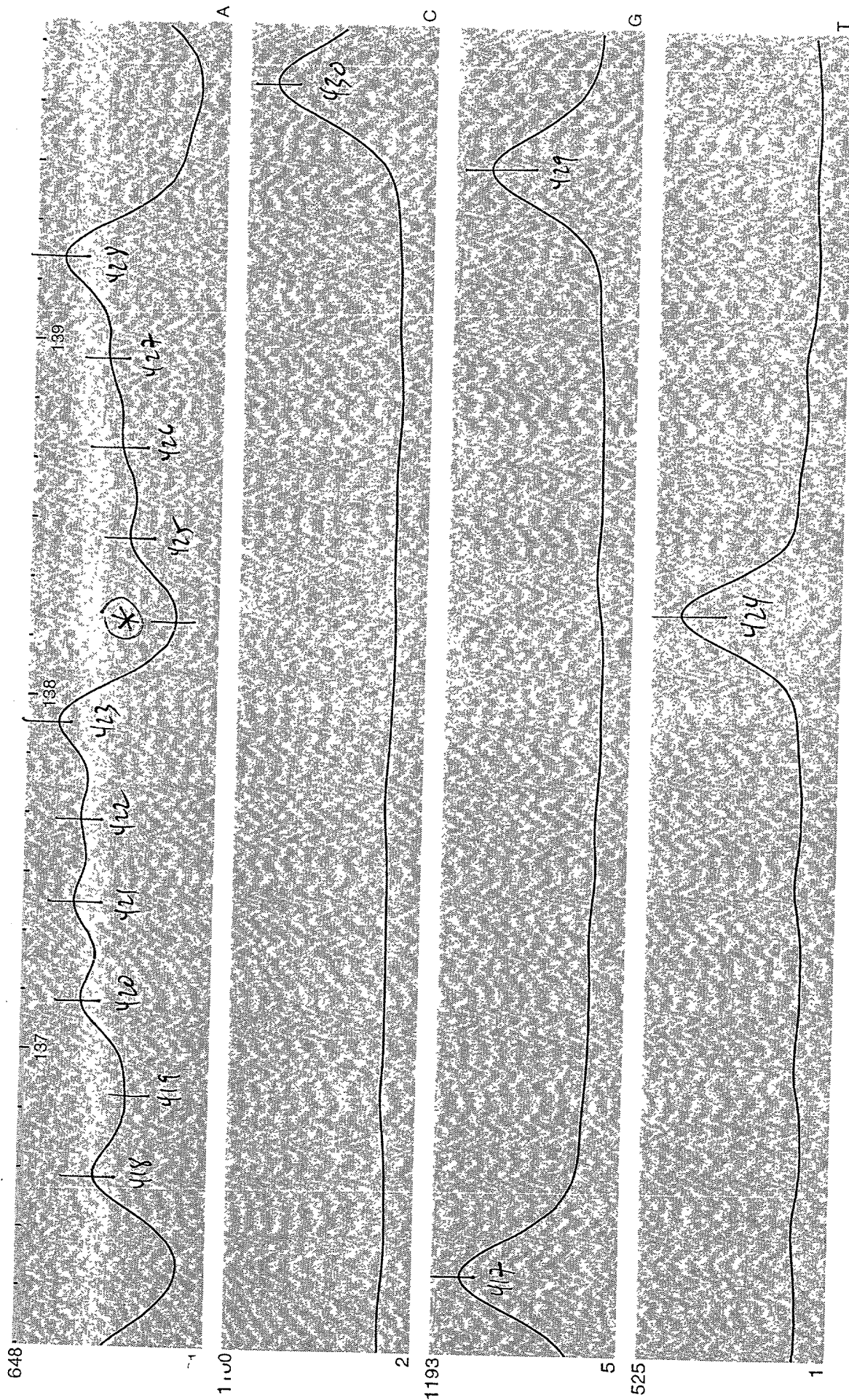
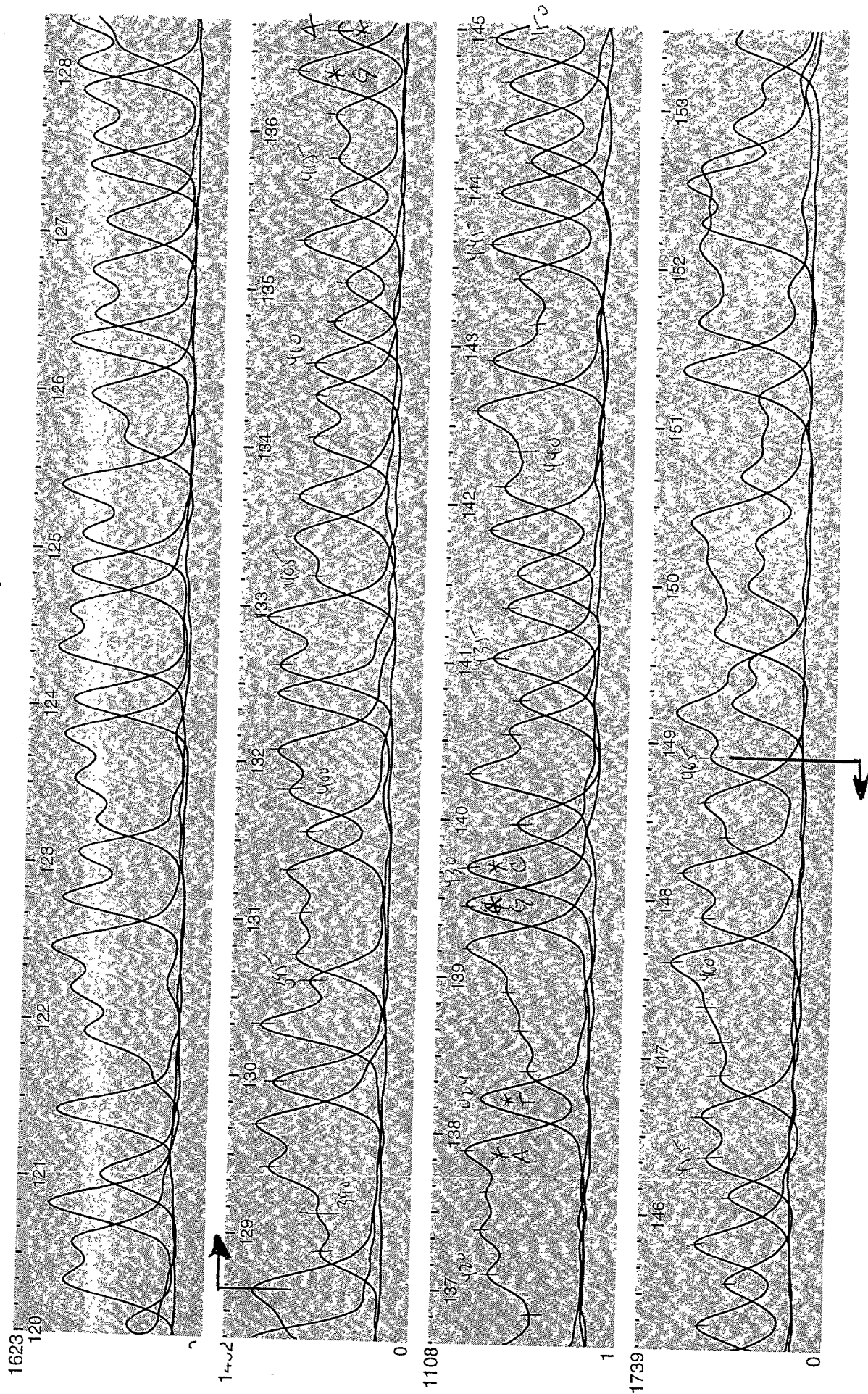


Figure 9Bc



Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc



Deviation of the peak position (in number of bases) from the average
as a function of base number in different traces before alignment

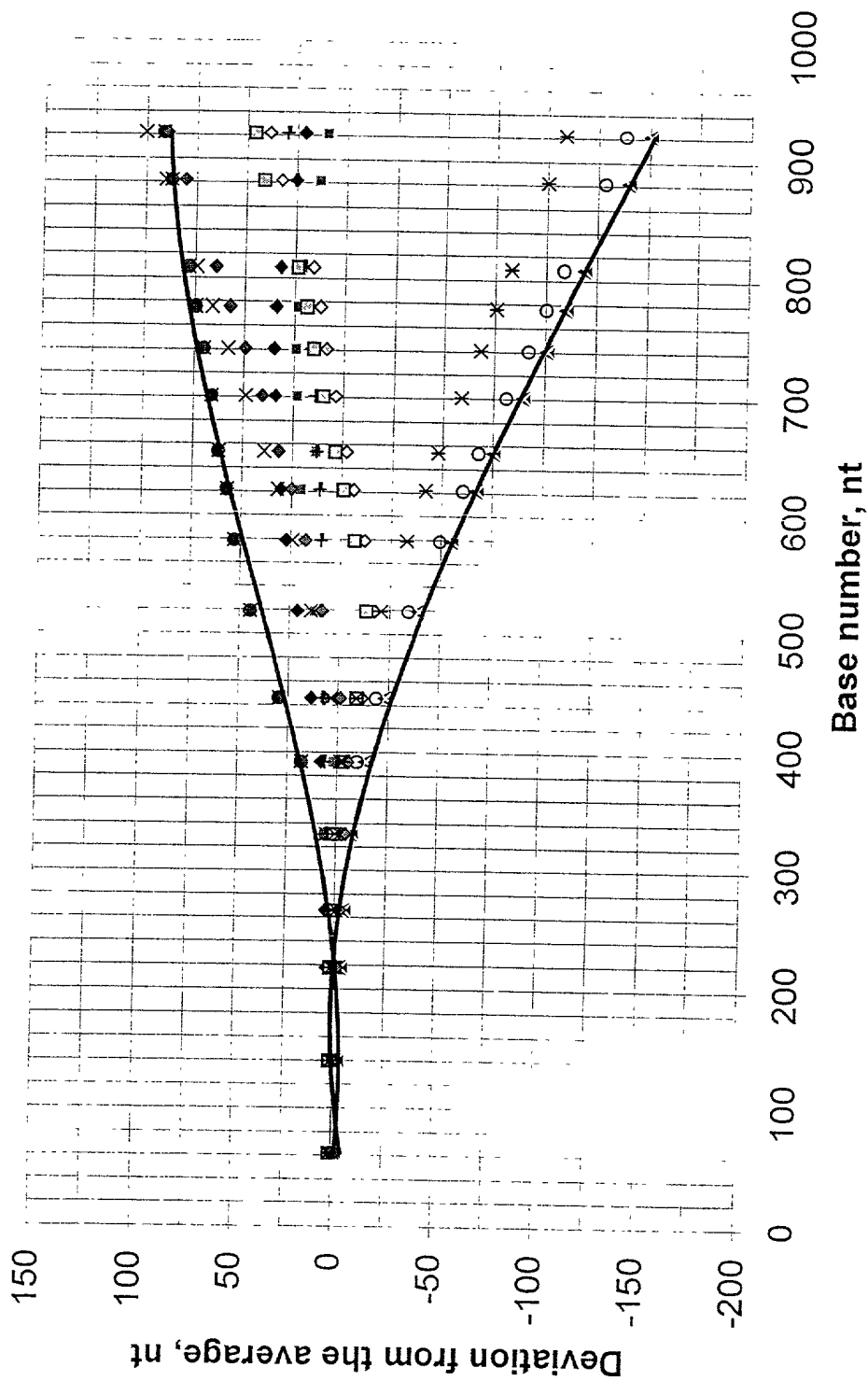


Figure 10

Deviation of the peak position (in number of bases) from the average
as a function of base number in the traces aligned with internal
standards
(long gel, M13, 5-th degree polynomial) 17 Ref. Peaks

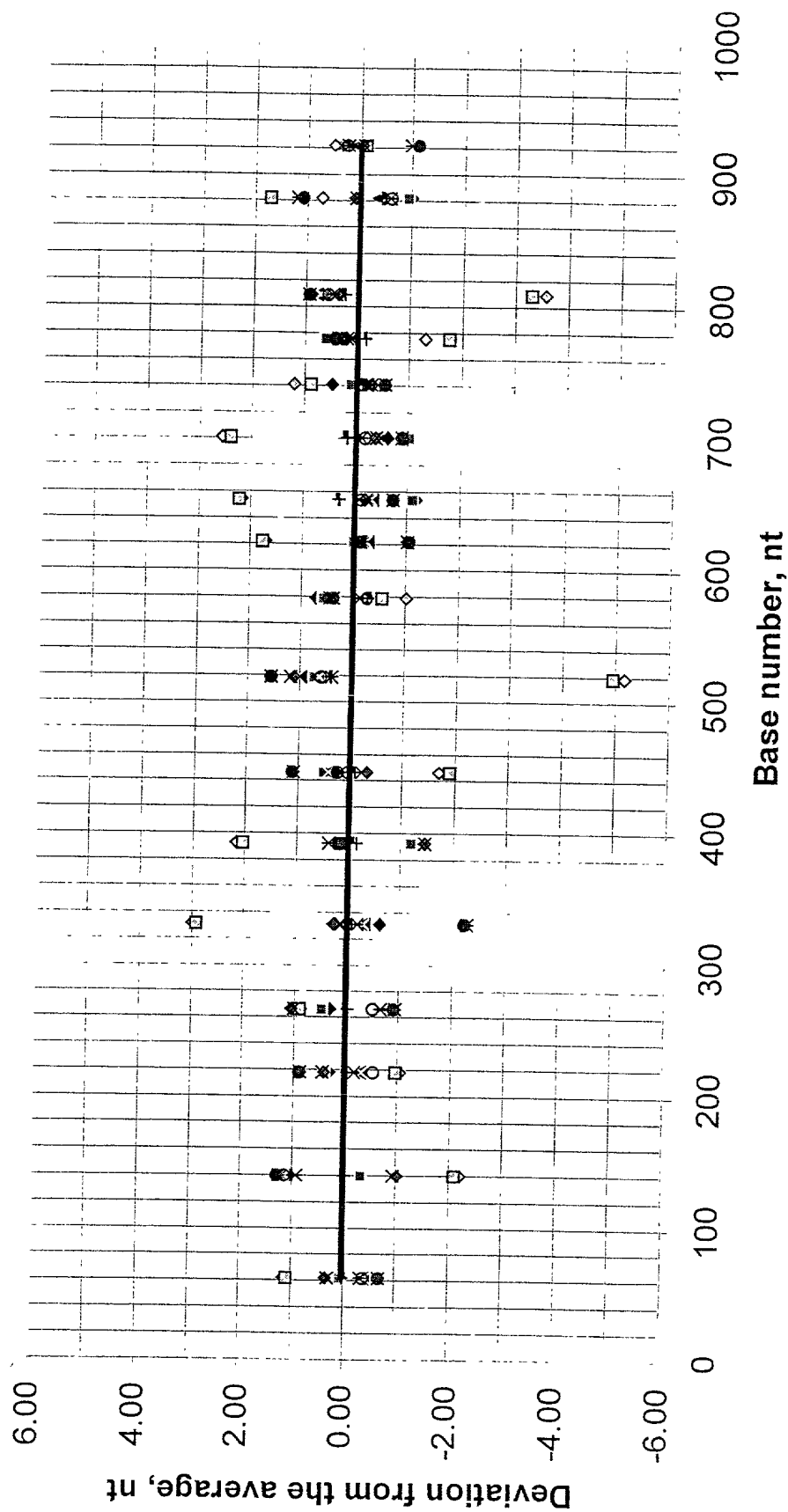


Figure 11

Deviation of the peak position from the average as a function of base number in the traces aligned with internal standards
(long gel, M13, 6 peaks, 5-th degree polynomial)

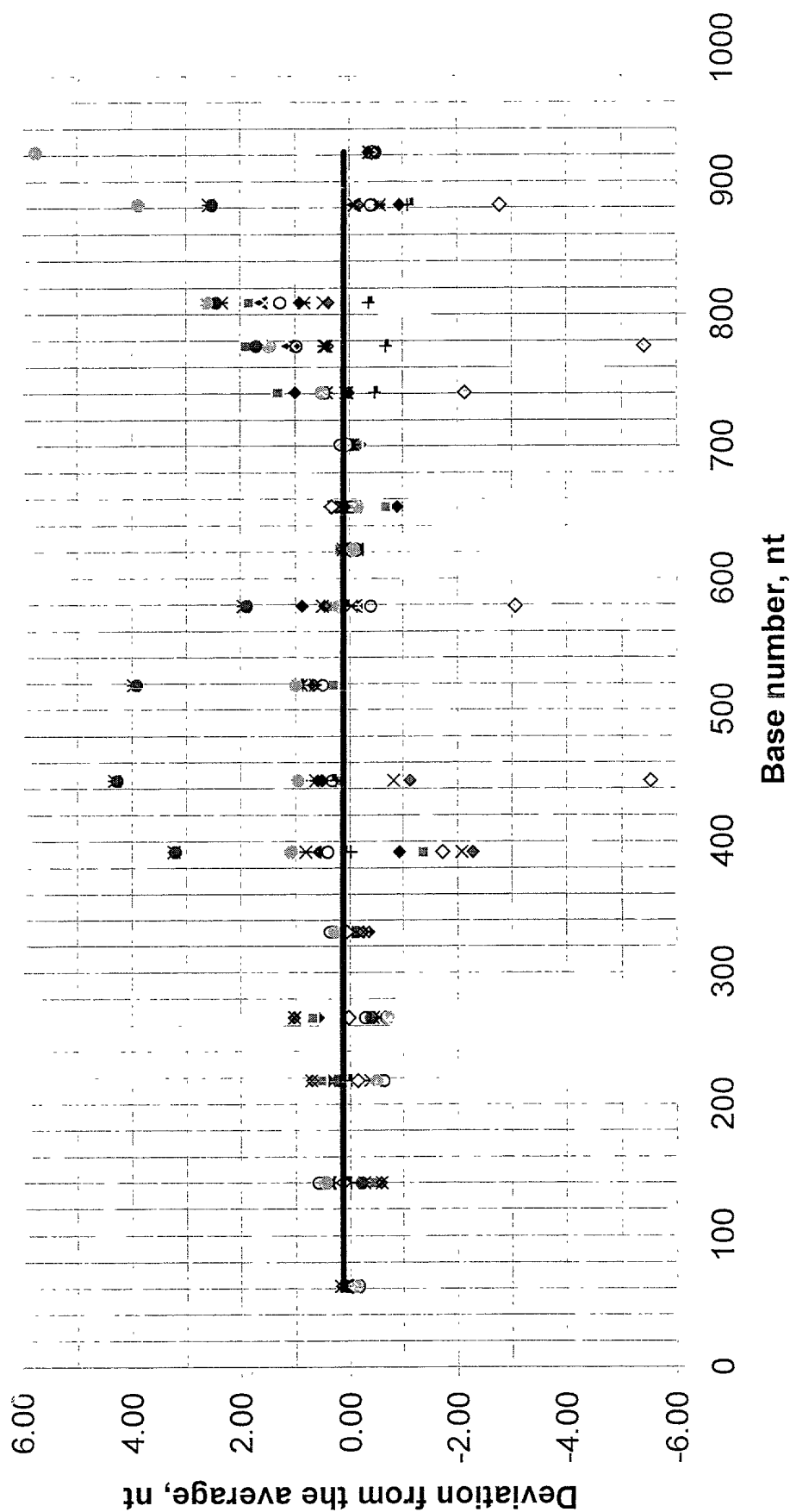


Figure 12